

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2003, 06:15:48 ; Search time 2313 Seconds

(without alignments)

10502.910 Million cell updates/sec

Title: US-09-043-944-5

Perfect score: 1500

Sequence: 1 gtttaattaccacgaatttga.....taaaaaaaaaaaaaaaaaaaaaa 1500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_man:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470.6	31.4	477	13	Bil174328
2	374	24.9	386	13	Bil175258
3	362	24.1	374	14	C66636
4	361.4	24.1	375	14	C47805
5	360	24.0	360	9	AV190680
6	350.6	23.4	360	9	AV186436

ALIGNMENTS

AV198059	AV198059	360	9	AV198059	23.3	350	7
AV192017	AV192017	374	9	AV192017	22.8	342.6	8
C39939	C39939	360	14	C39939	22.7	340.6	9
AV185173	AV185173	300	9	AV185173	19.1	287	10
C29641	C29641	300	14	C29641	19.1	286	11
C55887	C55887	300	14	C55887	19.0	285	12
AV178913	AV178913	300	9	AV178913	18.9	283.4	13
C29851	C29851	300	14	C29851	18.7	280.8	14
C35957	C35957	300	14	C35957	18.4	276.4	15
C34382	C34382	300	14	C34382	18.2	272.6	16
AV175978	AV175978	300	9	AV175978	17.9	268.8	17
AV179958	AV179958	300	9	AV179958	16.9	253.6	18
BM548100	BM548100	1101	13	BM548100	14.8	221.8	19
AI675803	AI675803	661	9	AI675803	14.6	219	20
AI925372	AI925372	703	9	AI925372	14.5	217.4	21
AK014706	AK014706	1998	11	AK014706	14.5	216.8	22
AI831581	AI831581	680	9	AI831581	14.2	212.6	23
AL553513	AL553513	1006	9	AL553513	13.9	207.8	24
AL553084	AL553084	977	9	AL553084	13.7	205.2	25
AW604230	AW604230	705	10	AW604230	13.6	204.2	26
AW850631	AW850631	733	10	AW850631	13.6	204.2	27
AW367465	AW367465	613	10	AW367465	13.6	203.8	28
AW604295	AW604295	640	10	AW604295	13.5	203.2	29
AW850640	AW850640	671	10	AW850640	13.5	202.6	30
AW604310	AW604310	714	10	AW604310	13.5	202.6	31
AW850636	AW850636	735	10	AW850636	13.5	202.6	32
AW850727	AW850727	573	10	AW850727	13.5	202.2	33
AW604307	AW604307	601	10	AW604307	13.4	201.6	34
AW850572	AW850572	757	10	AW850572	13.4	201.6	35
AW850573	AW850573	593	10	AW850573	13.4	201.4	36
AW604231	AW604231	599	10	AW604231	13.4	201.4	37
AW850632	AW850632	737	10	AW850632	13.4	200.4	38
AW850712	AW850712	581	10	AW850712	13.3	200	39
AW376912	AW376912	585	10	AW376912	13.3	200	40
AW604313	AW604313	592	10	AW604313	13.3	200	41
AW850561	AW850561	591	10	AW850561	13.3	198.8	42
AW367429	AW367429	588	10	AW367429	13.2	198.6	43
BF334085	BF334085	605	12	BF334085	13.2	198.4	44
AW850715	AW850715	570	10	AW850715	13.2	198.2	45
AW850639	AW850639	614	10	AW850639	13.2	197.8	46
AW376998	AW376998	584	10	AW376998	13.1	196.8	47
AW604233	AW604233	601	10	AW604233	12.8	191.6	48
AW367487	AW367487	590	10	AW367487	12.7	190.4	49
AW367418	AW367418	553	10	AW367418	12.6	189.4	50
BG288033	BG288033	827	12	BG288033	12.6	188.8	51
AW604271	AW604271	545	10	AW604271	12.6	188.6	52
AW850719	AW850719	544	10	AW850719	12.5	187.6	53
AW604298	AW604298	727	10	AW604298	12.5	187.6	54
AA993681	AA993681	587	9	AA993681	12.3	184.8	55
AW850575	AW850575	565	10	AW850575	12.3	184.6	56
AW850723	AW850723	544	10	AW850723	12.3	184.4	57
AW604272	AW604272	544	10	AW604272	12.2	183.4	58
AW376886	AW376886	551	10	AW376886	12.2	182.6	59
BG633935	BG633935	704	12	BG633935	12.1	182.2	60
AW52758	AW52758	689	10	AW52758	12.1	181.4	61
AW376995	AW376995	536	10	AW376995	12.1	181.2	62
AW850564	AW850564	660	10	AW850564	12.0	180.8	63
AW752760	AW752760	545	10	AW752760	12.0	180.6	64
AW850571	AW850571	645	10	AW850571	12.0	179.6	65
BE283320	BE283320	778	10	BE283320	11.8	176.8	66
AW52766	AW52766	650	10	AW52766	11.8	176.4	67
AW367547	AW367547	561	10	AW367547	11.7	175.8	68
AW52778	AW52778	646	10	AW52778	11.7	175.6	69
BI453842	BI453842	944	13	BI453842	11.7	175	70
AW376926	AW376926	654	10	AW376926	11.7	174.8	71
AW52773	AW52773	622	10	AW52773	11.6	173.6	72
BF334090	BF334090	555	12	BF334090	11.5	172.6	73
AL555434	AL555434	994	9	AL555434	11.4	171.6	75

```

RESULT 1
BI174328
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

BI174328
OSTF019E11_1 AD-wrmcDNA Caenorhabditis elegans cdna similar to
AAD50991, mRNA sequence.
BI174328
BI174328.1 GI:14640131
EST.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 477)
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-I, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
21135099
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome_Reboul@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@fci.harvard.edu or
philippe_vaglio@fci.harvard.edu
POLYA-No.
LOCATION/Qualifiers
1. .477
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="AD-wrmcDNA"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 131 a 87 c 109 g 150 t
ORIGIN
Query Match 31.4%; Score 470.6; DB 13; Length 477;
Best Local Similarity 99.2%; Pred. No. 7.7e-72;
Matches 473; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 41 AACAGGAGCGGAGGTGCAGATCGCGAACAACATACCGTTACGGTACAAATCTGATAA 100
|||||
Db 1 AACAGGAGCGGAGGTGCAGATCGCGAACAACATACCGTTACGGTACAAATCTGATAA 60
|||||
QY 101 CAATCCGAATAGCCAAAGACAGCAAAATCTGTGGAAGAGCGGAGCTGAAATACGGAG 160
|||||
Db 61 CAATCCGAATAGCCAAAGACAGCAAAATCTGTGGAAGAGCGGAGCTGAAATACGGAG 120
|||||
QY 161 CATCTCAGTTATTCATCTATTTGTGCGGTGTCACATGATGCATGGCTCTGGTTGTTTAA 220
|||||
Db 121 CATCTCAGTTATTCATCTATTTGTGCGGTGTCACATGATGCATGGCTCTGGTTGTTTAA 180
|||||
QY 221 CGATGACAGATACGTTTTATAGTCAAAACATGGAAGCATTTACTATCATACCCCTT 280
|||||
Db 181 CGATGACAGATACGTTTTATAGTCAAAACATGGAAGCATTTACTATCATACCCCTT 240
|||||
QY 281 TTGTCCGGGAAACAGACAGTATCGTTGAGAAGGGATTGATGTCACCTTGGAAATGCTCTCG 340
|||||

```

```

Db 241 TTGTCCGGGAAACAGACAGTATCGTTGAGAAGGGATTGATGTCACTTGGAAATGCTCTCG 300
QY 341 TCATGTTGTGCGGTGCTGTTCTGATGACAGTCTGCTGATGTTCTTCTATAAATAACAAGT 400
|||||
Db 301 TCATGTTGTGCGGTGCTGTTCTGATGACAGTCTGCTGATGTTCTTCTATAAATAACAAGT 360
|||||
QY 401 TTTATAAGCTTATTCATGATGATGGCTTATTCGACAGTCTTCTCTCTCTCTCTCTCTCTCTCT 460
|||||
Db 361 TTTATAAGCTTATTCATGATGATGGCTTATTCGACAGTCTTCTCTCTCTCTCTCTCTCTCTCT 420
|||||
QY 461 CTCAATCTATGTCGAAGAAGTCTGAAAAGTTTCGATGTTGCTCCAGCGCACTAT 517
|||||
Db 421 CTCAATCTATGTCGAAGAAGTCTGAAAAGTTTCGATGTTGCTCCAGCGCACTAT 477
|||||

RESULT 2
BI175258/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

BI175258
OSTR019E11_1 AD-wrmcDNA Caenorhabditis elegans cdna similar to
AAD50991, mRNA sequence.
BI175258
BI175258.1 GI:14641061
EST.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 386)
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-I, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.,
Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
21135099
Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome_Reboul@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@fci.harvard.edu or
philippe_vaglio@fci.harvard.edu
POLYA-No.
LOCATION/Qualifiers
1. .386
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="AD-wrmcDNA"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
BASE COUNT 108 a 82 c 100 g 96 t
ORIGIN
Query Match 24.9%; Score 374; DB 13; Length 386;
Best Local Similarity 99.7%; Pred. No. 4.2e-55;
Matches 385; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 937 AAAGTGAACGAATTCCTCAAAAAGTCAAAATCGAATCGAATCTACAGTTCACAGACA 996
|||||
Db 386 AAAGTGAACGAATTCCTCAAAAAGTCAAAATCGAATCGAATCTACAGTTCACAGACA 327
|||||

```

Db 61 CTCGTCATGTTGTGGCTGGTCTCTGATGACACAGTCTGCTCATTTGTTTTCTATAAATAC 120

C47805	375 bp	mrna	linear	EST 18-OCT-1999
C47805	Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo			
C47805	Caenorhabditis elegans cDNA clone yk452b9 5', mRNA sequence.			
C47805	GI:2384058			
EST.				
Caenorhabditis elegans.				
Caenorhabditis elegans				
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhaditida; Rhaditoidaea				
: Rhaditidae; Pelodirinae; Caenorhabditis.				
1 (bases 1 to 375)				
Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano				
,M., Miyata,A. and Nishigaki,A.				
Expression map of the C.elegans genome				
Unpublished (1996)				
Contact: Yuji Kohara				
Genome Biology Lab.				
National Institute of Genetics				
Yata 1111, Mishima, Shizuoka 411, Japan				
Tel: 81-559-81-6854				
Fax: 81-559-81-6855				
Email: ykohara@lab.nig.ac.jp.				
Location/Qualifiers				
1. .375				
/organism="Caenorhabditis elegans"				
/strain="N2"				
/db_xref="taxon:6239"				
/clone="yk452b9"				
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2				
hermaphrodite embryo"				
/sex="hermaphrodite"				
/dev_stage="embryo"				
BASE COUNT	99 a	95 c	81 g	100 t
ORIGIN				
Query Match	24.1%;	Score 361.4;	DB 14;	Length 375;
Best Local Similarity	99.5%;	Pred. No. 6.5e-53;		
Matches 373;	Conservative	0;	Mismatches 1;	Indels 1;
Gaps 1;				
Qy	921	AAAGCCAAAACGCCCAAAAGCTGAACCAAAATTCCTCAAAAAGTCCAAATCGAATTC	980	
Db	1	AAAGCCAAAACGCCCAAAAGCTGAACCAAAATTCCTCAAAAAGTCCAAATCGAATTC	60	
Qy	981	TACAGCTTCAACGACACAAAACTCTGGAGTAAAGGTGGAACGGGAGCTAGCTGCTGAGAG	1040	
Db	61	TACAGCTTCAACGACACAAAACTCTGGAGTAAAGGTGGAACGGGAGCTAGCTGCTGAGAG	120	
Qy	1041	ACCAACTGTACAAGACGCCCAATTTTCACGGCAGCAAGAGAGAGAGGCTGTGAAACT	1100	

QY 292 ACAGACAGTACGCTTGAGAGGAGTGTGATGTCACCTTGGAAGCTCTCGTCATGTTGTGC 351
|||||
Db 242 ACAGACAGTACGCTTGAGAGGAGTGTGATGTCACCTTGGAAGCTCTCGTCATGTTGTGC 301
|||||
QY 352 GTGGTCTGCTGATGACAGTTCGCTGATGTTCTTATATAAATACAACTTTTATAAGCT 410
|||||
Db 302 GTGGTCTGCTGATGACAGTTCGCTGATGTTCTTATATAAATACAACTTTTATAAGCT 360
|||||

RESULT 7
LOCUS AV198059 360 bp mRNA linear EST 26-JUL-1999
DEFINITION AV198059 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk674e3 5', mRNA sequence.

ACCESSION AV198059.1 GI:5581830
VERSION
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Shin-i.T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano ,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.

TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source
1. .360
Location/Qualifiers
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="yk674e3"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"

BASE COUNT 103 a 63 c 89 g 103 t 2 others
ORIGIN

Query Match 23.3%; Score 350; DB 9; Length 360;
Best Local Similarity 98.1%; Pred. No. 6.2e-51;
Matches 353; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 41 AACAGAGGCGGAGGTGCAGATGCGGAACACATACCGTTTACGGTACAAATCTGATAA 100
|||||
Db 1 AACAGAGGCGGAGGTGCAGATGCGGAACACATACCGTTTACGGTACAAATCTGATAA 60
|||||

QY 101 CAAATCGAATAGCCAGAGACGAAATCTGTGGAAGACGGAGCTGAAATACGGAG 160
|||||
Db 61 CAAATCGAATAGCCAGAGACGAAATCTGTGGAAGACGGAGCTGAAATACGGAG 120
|||||

QY 161 CATCTCAGTTATTCATCTATTTGTGCGGCTGTCATGATGATGCTGCTGTTGTTTAA 220
|||||
Db 121 CATCTCAGTTATTCATCTATTTGTGCGGCTGTCATGATGATGCTGCTGTTGTTTAA 180
|||||

QY 221 CGATGACAGGATACGTTTATAGTCAAAACATGGAAGGCATTACTATCATCATCCTT 280
|||||
Db 181 CGATGACAGGATACGTTTATAGTCAAAACATGGAAGGCATTACTATCATCATCCTT 240
|||||

QY 281 TTGTCCGGGAAACACAGACAGTATCGTTGAGAAGGATTTGATGTCACCTTGGAATGCTCTCG 340
|||||
Db 241 TTGTCCGGGAAACACAGACAGTATCGTTGAGAAGGATTTGATGTCACCTTGGAATGCTCTCG 300
|||||

QY 341 TCATGTTGTGCGGTGCTTCTGATGACAGTCTCTGCTGATTTGTTTCTATAAATACAAAGT 400
|||||

Db 301 TCATGTTGTGCGGTGCTTCTGATGACAGTCTCTGCTGATGTTTCTTATAAATACAAAGT 360
|||||

RESULT 8
LOCUS AV192017 374 bp mRNA linear EST 22-JUL-1999
DEFINITION AV192017 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk600e12 5', mRNA sequence.

ACCESSION AV192017.1 GI:5574169
VERSION
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 374)
AUTHORS Kohara,Y., Shin-i.T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano ,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.

TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source
1. .374
Location/Qualifiers
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="yk600e12"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"

BASE COUNT 109 a 63 c 91 g 111 t
ORIGIN

Query Match 22.8%; Score 342.6; DB 9; Length 374;
Best Local Similarity 98.4%; Pred. No. 1.1e-49;
Matches 367; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 44 AGGAGGCGGAGGTGCAGATGCGG-AAACACATACCGTTTACGGTACAAATCTGATAACA 102
|||||
Db 2 AGGAGGCGGAGGTGCAGATGCGGAAACACATACCGTTTACGGTACAAATCTGATAACA 61
|||||

QY 103 AATCGG-AATAGCCAGAGACGAAATGTTGTGGAAGACGGAGCTGAAATACGGAGC 161
|||||
Db 62 AATCGGAAATAGCCAGAGACGAAATGTTGTGGAAGACGGAGCTGAAATACGGAGC 121
|||||

QY 162 ATCTCAGTTATTCATCTATTTGTGCGGCTGTCACATGATGATGCTGCTGTTGTTTAC 221
|||||
Db 122 ATCTCAGTTATTCATCTATTTGTGCGGCTGTCACATGATGATGCTGCTGTTGTTTAC 181
|||||

QY 222 GATGAACACGATTACGTTTATAGTCAAAACATGGAAGGCATTACTATCATCATCCTT 281
|||||
Db 182 GATGAACACGATTACGTTTATAGTCAAAACATGGAAGGCATTACTATCATCATCCTT 241
|||||

QY 282 TGTCGGGAAACACAGACAGTATCGTTGAGAAGGATTCATGTCACCTTGGAAATGCTCTCGT 341
|||||
Db 242 TGTCGGGAAACACAGACAGTATCGTTGAGAAGGATTCATGTCACCTTGGAAATGCTCTCGT 301
|||||

QY 342 CATGTTGCTGCTGCTGCTGCTGATGACAGTTCCTGCTGATTTGTTTCTATAAATACAAAGT 401
|||||
Db 302 CATGTTGCTGCTGCTGCTGCTGATGACAGTTCCTGCTGATTTTCTATAAATACAAAGT 361
|||||

QY 402 TTATAAGCTTATT 414
|||||

```
Db 362 TTTAAGCTTATT 374
|||||
C39939 360 bp mRNA linear EST 18-OCT-1999
C39939 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo
Caenorhabditis elegans cDNA clone yk221d3 5', mRNA sequence.
C39939
ACCESSION C39939.1 GI:2376176
VERSION C39939
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES
source
1..360
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT 104 a 63 c 90 g 102 t 1 others
ORIGIN
Query Match 22.7%; Score 340.6; DB 14; Length 360;
Best Local Similarity 98.8%; Pred. No. 2.6e-49;
Matches 354; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 37 AGACAACAGAGGCGGAGGTGCAGATGCGG-AAACACATACCGTTTACGGTACAATCT 95
|||||
Db 2 AGACAACAGAGGCGGAGGTGCAGATGCGGAAACACATACCGTTTACGGTACAATCT 61
|||||
QY 96 GATAACAATTCGGAATAGCCAGAGACGAAATGTTGGAGAGCGGAGCTGAATA 155
|||||
Db 62 GATAACAATTCGGAATAGCCAGAGACGAAATGTTGGAGAGCGGAGCTGAATA 121
|||||
QY 156 CGGAGATCTCAGTTTATCATCTATTGTCGGGTGTCACATGATGCTGCTGTTGT 215
|||||
Db 122 CGGAGATCTCAGTTTATCATCTATTGTCGGGTGTCACATGATGCTGCTGTTGT 181
|||||
QY 216 TTTTACGATGAACACGATTACGTTTATAGTCAAAACAATGGAAGCATTACTATCAC 275
|||||
Db 182 TTTTACGATGAACACGATTACGTTTATAGTCAAAACAATGGAAGCATTACTATCAC 241
|||||
QY 276 TCTTTTTCGCGGAAACAGACAGTATCGTTGAGAGGATTGATGCTCACTTGGAAATGC 335
|||||
Db 242 TCTTTTTCGCGGAAACAGACAGTATCGTTGAGAGGATTGATGCTCACTTGGAAATGC 301
|||||
QY 336 TCTCGTCATGTCGCGTCTGTCATGATGACAGTTCGTCGATGTTTCTATAAAT 394
|||||
Db 302 TCTCGTCATGTCGCGTCTGTCATGATGACAGTTCGTCGATGTTTCTATAAAT 360
|||||
RESULT 10
AV185173/c 300 bp mRNA linear EST 21-JUL-1999
LOCUS AV185173
DEFINITION
C29641 300 bp mRNA linear EST 18-OCT-1999
C29641 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo
Caenorhabditis elegans cDNA clone yk216el 3', mRNA sequence.
C29641
ACCESSION C29641.1 GI:2361437
VERSION C29641
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
REFERENCE 1 (bases 1 to 300)
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A., Mitani,Y., Iida,K., Desugi,H., Sugiyama,Y. and
Nomoto,H.
TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES
source
1..300
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT 117 a 44 c 83 g 55 t 1 others
ORIGIN
Query Match 19.1%; Score 287; DB 9; Length 300;
Best Local Similarity 99.3%; Pred. No. 5.2e-40;
Matches 298; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1116 CATTTCCTACTCTGTTCTCTCGCAAGGCTTCATCGTACTTGTGCTGCGGCTAT 1175
|||||
Db 300 CATTTCCTACTCTGTTCTCTCGCAAGGCTTCATCGTACTTGTGCTGCGGCTAT 241
|||||
QY 1176 CGCTTGTATGTGGCCATTCTTATCGTCTCTGTTCACTTGTCTGCTGCGGCTCT 1235
|||||
Db 240 CGCTTGTATGTGGCCATTCTTATCGTCTCTGTTCACTTGTCTGCTGCGGCTCT 181
|||||
QY 1236 CAAACGAGACCTCCCGGCTCTG-CAATTTCCATTTTCTCCGACTCATTTTTTAC 1294
|||||
Db 180 CAAACGAGACCTCCCGGCTCTGCCAATTTCCATTTTCTCCGACTCATTTTTTAC 121
|||||
QY 1295 TACCGCTCGATCACCACCCCATTTGTTACACAGTCTCTCAAAAGTGTATTATTA 1354
|||||
Db 120 TACCGCTCGATCACCACCCCATTTGTTACACAGTCTCTCAAAAGTGTATTATTA 61
|||||
QY 1355 ATTCTCTGTTTGTGCAATTTCTTGCATCATCAACTTTTTCGATTATATCTTGAG 1414
|||||
Db 60 ATTCTCTGTTTGTGCAATTTCTTGCATCATCAACTTTTTCGATTATATCTTGAG 1
```

REFERENCE 1 (bases 1 to 300)
 AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
 TITLE M., Miyata,A. and Nishigaki,A.
 JOURNAL Expression map of the C.elegans genome
 COMMENT Unpublished (1996)
 CONTACT: Yuji Kohara
 Genomic Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp.
 Location/Qualifiers
 1. .300
 /organism="Caenorhabditis elegans"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone="yk216el"
 /clone_lib="Yuji Kohara unpublished cDNA:Strain N2
 hermaphrodite embryo"
 /sex="hermaphrodite"
 /dev_stage="embryo"
 /dev_stage="embryo"

BASE COUNT 118 a 44 c 81 g 56 t 1 others
 ORIGIN
 Query Match 19.1%; Score 286; DB 14; Length 300;
 Best Local Similarity 99.3%; Pred.No: 7.7e-40;
 Matches 297; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 1114 TTCAATTTCTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTGGACAGACT 1173
 |||||
 299 TTCAATTTTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTGGACAGACT 240
 |||||
 1174 ATCGCTGTGATGCGCATTCATCGTCTCTGCTTCACTCTTCTGCTGCTGCGGTC 1233
 |||||
 239 ATCGCTGTGATGCGCATTCATCGTCTCTGCTTCACTCTTCTGCTGCTGCGGTC 180
 |||||
 1234 TTCAACAGGACACTCCCGGCTCTG-CAATTTCCATTTTCTCGGACTCAATTTTACTTT 1292
 |||||
 179 TTCAACAGGACACTCCCGGCTCTG-CAATTTCCATTTTCTCGGACTCAATTTTACTTT 120
 |||||
 1293 TGTACCGCTGGATCATCCCCATTTGTACACAGTCTCACAAGTGTATTATATAT 1352
 |||||
 119 TGTACCGCTGGATCATCCCCATTTGTACACAGTCTCACAAGTGTATTATATAT 60
 |||||
 1353 TAATCTCTGTTTGGCAATTTCTTGCATCATCAACTTTTCGATTATATCTTGAGCGA 1411
 |||||
 59 TAATCTCTGTTTGGCAATTTCTTGCATCATCAACTTTTCGATTATATCTTGAGCGA 1

RESULT 12
 C55887/c
 LOCUS 300 bp mRNA linear EST 16-SEP-1997
 DEFINITION. C55887 Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA
 clone yk231a7 3', mRNA sequence.
 C55887
 VERSION C55887.1 GI:2400488
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.
 1 (bases 1 to 300)
 Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
 M., Miyata,A. and Nishigaki,A.
 TITLE Expression map of the C.elegans genome
 JOURNAL Unpublished (1996)
 COMMENT Contact: Yuji Kohara
 Genomic Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855

Email: ykohara@lab.nig.ac.jp.
 Location/Qualifiers
 1. .300
 /organism="Caenorhabditis elegans"
 /strain="CB1489 him-8(el489)"
 /db_xref="taxon:6239"
 /clone="yk231a7"
 /clone_lib="Yuji Kohara unpublished cDNA"
 /sex="hermaphrodite, male"
 /tissue_type="whole animal"
 /dev_stage="varied"

BASE COUNT 116 a 44 c 81 g 56 t 3 others
 ORIGIN
 Query Match 19.0%; Score 285; DB 14; Length 300;
 Best Local Similarity 98.7%; Pred.No: 1.2e-39;
 Matches 296; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 1119 TTCTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTGGACAGACTATCGC 1178
 |||||
 300 TTCTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTGGACAGACTATCGC 241
 |||||
 1179 TTCTTATGCGCATTCATTATCGTCTCTGCTTCACTCTTCTGCTGCTGCGGCTCTCAA 1238
 |||||
 240 TTCTTATGCGCATTCATTATCGTCTCTGCTTCACTCTTCTGCTGCTGCGGCTCTCAA 181
 |||||
 1239 ACAGACACTCCCGGCTCTG-CAATTTCCATTTTCTCGGACTCATTTTACTTTTGTAC 1297
 |||||
 180 ACAGACACTCCCGGCTCTG-CAATTTCCATTTTCTCGGACTCATTTTACTTTTGTAC 121
 |||||
 1298 CGCTCGATCATCACCCCATTTTGTACACAGTCTCTCAAAGTGTATTATATTAATT 1357
 |||||
 120 CGCTCGATCATCACCCCATTTTGTACACAGTCTCTCAAAGTGTATTATATTAATT 61
 |||||
 1358 CTCTGTTTGGCAATTTCTTGCATCATCAACTTTTCGATTATATCTTGAGCGATCTCAA 1417
 |||||
 60 CTCTGTTTGGCAATTTCTTGCATCATCAACTTTTCGATTATATCTTGAGCGATCTCAA 1

RESULT 13
 AV178913/c
 LOCUS 300 bp mRNA linear EST 21-JUL-1999
 DEFINITION AV178913 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
 embryo Caenorhabditis elegans CDNA clone yk573h4 3', mRNA sequence.
 AV178913
 VERSION AV178913.1 GI:5558814
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
 ; Rhabditidae; Peloderinae; Caenorhabditis.
 1 (bases 1 to 300)
 Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
 Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano
 M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
 Nomoto,H.
 TITLE Expressed genes in C.elegans
 JOURNAL Unpublished (1999)
 COMMENT Contact: Yuji Kohara
 Genomic Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp.
 Location/Qualifiers
 1. .300
 /organism="Caenorhabditis elegans"
 /strain="N2"
 /db_xref="taxon:6239"
 /clone="yk573h4"
 /clone_lib="Yuji Kohara unpublished cDNA:Strain N2
 hermaphrodite embryo"

```

/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT      118 a      44 c      79 g      56 t      3 others
ORIGIN

Query Match      18.9%; Score 283.4; DB 9; Length 300;
Best Local Similarity 98.3%; Pred. No. 2.2e-39;
Matches 293; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1118 TTCTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTTGAACACGACTATCG 1177
DDB 300 TTTTATCTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTTGAACACGACTATCG 241
QY 1178 CTGTTATGCGCATCTTATCGGCTCTGCTTCGTTCTGCTCTGCTCGGCTCTTCA 1237
DDB 240 CTGTTATGCGCATCTTATCGGCTCTGCTTCGTTCTGCTCTGCTCGGCTCTTCA 181
QY 1238 AAGGACACATCCCGGCTCTG-CAATTCGATCTTCTCCGACATCTTTTACTTTGTA 1296
DDB 180 AAGGACACATCCCGGCTCTGCAATTCGATCTTCTCCGACATCTTTTACTTTGTA 121
QY 1297 CCGCTGGATCATCACCCCATTTGTTACACAAGTCTCTCAAAAGTGTATTATTAAT 1356
DDB 120 CCGCTGGATCATCACCCCATTTGTTACACAAGTCTCTCAAAAGTGTATTATTAAT 61
QY 1357 TCCTGTTGTTGCAATCTTTTCATCATCACTTTTCGATTTATCTTGGAGCATCTCA 1416
DDB 60 TCCTGTTGTTGCAATCTTTTCATCATCACTTTTCGATTTATCTTGGAGCATCTCA 1

RESULT 14
C29851/c
LOCUS
DEFINITION
C29851 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo
Caenorhabditis elegans cDNA clone yk221d3 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
AUTHORS
Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A. and Nishigaki,A.
TITLE
Expression map of the C.elegans genome
JOURNAL
Unpublished (1996)
COMMENT
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .300
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT      116 a      44 c      80 g      56 t      4 others
ORIGIN

Query Match      18.7%; Score 280.8; DB 14; Length 300;
Best Local Similarity 97.7%; Pred. No. 6.1e-39;
Matches 293; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1119 TTCTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTTGAACACGACTATCG 1178
DDB 111 TTTTATCTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTTGAACACGACTATCG 1178

/sex="hermaphrodite"
/dev_stage="embryo"
BASE COUNT      118 a      44 c      79 g      56 t      3 others
ORIGIN

Query Match      18.4%; Score 276.4; DB 14; Length 300;
Best Local Similarity 99.3%; Pred. No. 3.5e-38;
Matches 288; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1114 TTCATTTTCTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTTGAACACGACT 1173
DDB 290 TTCATTTTCTACTCTGTTCTCTCGGCAAGGCTTCATCGTACTTTGACTTGAACACGACT 231
QY 1174 ATCGCTTGTATGTGCGCATCTTATCGGCTCTGCTTCTGCTCTGCTCTGCTCTGCTCTGCT 1233
DDB 230 ATCGCTTGTATGTGCGCATCTTATCGGCTCTGCTTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 171
QY 1234 TTCAACACGACACTCCCGGCTCTG-CAATTTCCATTTTCTCGGACTCATTTTACTTTT 1292
DDB 170 TTCAACACGACACTCCCGGCTCTGCAATTTCCATTTTCTCGGACTCATTTTACTTTT 111
QY 1293 TGATACCGCTGGATCATCACCCCATTTGTTACACAAGTCTCTCAAAAGTGTATTATTAAT 1352

```


REFERENCE 1 (bases 1 to 300)
AUTHORS Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H., Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Nomoto,H.
TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source
1..300
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk600e12"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"

BASE COUNT 115 a 44 C 66 G 67 T 8 others
ORIGIN
Query Match 16.9%; Score 253.6; DB 9; Length 300;
Best Local Similarity 92.5%; Pred. No. 3.1e-34;
Matches 273; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 1139 GCAGGCTTCATCGTACTTTGACTGGACACGACTATCGTGTGTTATGTCGCAATTTTA 1198
Db 295 GGNAGGNTTATTGNAATTTGAATGGAAAANGAATATCGTGTGTTATGTCGCAATTTTA 236
QY 1199 TCGGTCTCTGCTTCACTCTTGTCTGCTGCTGCTGCTTCAACAGCAGCACTCCCGGCTCG- 1257
Db 235 TCGGTNTATGNTTCACTCTGCTGCTGCTGCTGCTGCTTCAACAGCAGCACTCCCGGCTCG 176
QY 1258 CAATTTCCATTTTCTCGGACTCATTTTACATTTTGTACCGCTGGATCATCACCCCAT 1317
Db 175 CAATTTCCATTTTCTCGGACTCATTTTACATTTTGTACCGCTGGATCATCACCCCAT 116
QY 1318 TTGTTACACAGTCTCTCAAGCTGTTTATATATATATATATATATATATATATATATATAT 1377
Db 115 TTGTTACACAGTCTCTCAAGCTGTTTATATATATATATATATATATATATATATATATAT 56
QY 1378 TGCATCATCAACTTTTCGATATATATCTTGAGCGATCTCAAGCTTTTATTTACAT 1432
Db 55 TGCATCATCAACTTTTCGATATATATCTTGAGCGATCTCAAGCTTTTATTTACAT 1

RESULT 19
BM548100
LOCUS 1101 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6531717 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5732941
5', mRNA sequence.
ACCESSION BM548100
VERSION 1
KEYWORDS GI:18782416
SOURCE EST.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1101)
NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabps-re@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM12735 row: n column: 14
High quality sequence start: 9
High quality sequence stop: 643.
Location/Qualifiers
1..1101

source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5732941"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcorV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-df primed and directionally cloned (EcorV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
BASE COUNT 215 a 313 c 317 g 256 t
ORIGIN

Query Match 14.8%; Score 221.8; DB 13; Length 1101;
Best Local Similarity 59.4%; Pred. No. 4.8e-29;
Matches 395; Conservative 0; Mismatches 267; Indels 3; Gaps 1;

QY 135 GGAAGAAGCGAGCTGAAATACGAGCATCTACGTTATTTCATCTATTTTGTGCGGTGTC 194
Db 39 GAATGAGCTGACCTCAAAATACGGAAGCAGTGATCATGCTGTTTGTGCTGTGCAC 98
QY 195 ACTATGATGGCTCTGGTGTGTTTACGATGACACGATTTACGTTTATAGTCAAAACAA 254
Db 99 TCTGTGATGATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 158
QY 255 TGAAGAAGCAATTTACTATCATCTCTTTTGTCCGGGAAACAGACAGTATCTTCAGAGGG 314
Db 159 TGGACAGC---TCATCTACACGCCATTCATCTGAGGACACACCTCGGTGGCCAGCGCCT 215
QY 315 ATTGATGTCATCTGGAAATGCTCTCGTCATCTGTTGCGTGGTGGTGGTGGTGGTGGTGGT 374
Db 216 CCTCAACTCGCTGCTGAACACCTCATCATGATGATGATGATGATGATGATGATGATGAT 275
QY 375 GCTGATGTTTCTTCTATAAATACAAAGTTTATAGCTTATTCATGGATGGCTTATTGTCAG 434
Db 276 CTTGGTGGTGGTCTACAAGTACCGCTGTACAAGTTTCAATCCATCGGTGGTGGTGGTGGT 335
QY 435 CAGTTTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 494
Db 336 TTCACGTGATGCTGCT 395
QY 495 CGATGTCCTCCAGCGCACTATTGTTTGTGTTGAGTGGGTAACATATGAGTGTCTCGG 554
Db 396 CAATGTGGCCATGGACTACCCCTCTTGTGACTGTGTGAACTTCCGAGCTGGGCACTGGG 455
QY 555 AATGATGTCATACATTTGAAAGGTCATTCGCTCTGCAACAGTTCCTACCTTATTACAT 614
Db 456 CATGTTGTCATCCACTGGAGGGCCCTCTGTTGCTGACGAGCGCTACTCTCATCATGAT 515
QY 615 GTCTGCATTAATGGCTCTGCTCTTTTATCAAGTACCTTACCAGATGAGTGTGTGGTTTGT 674
Db 516 CAGTGGCTCATGGCCCTAGTGTTCATCAAGTACCTCCAGAGTGTGTCGCGTGGTGCAT 575
QY 675 GCTGTTTGTATCTCGTTTGGGATCTGTTGCGGTGCTCACACCAAAAGGACCAATGAG 734
Db 576 CCTGGGCGCCATCTCTGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 635
QY 735 ATATTGTTGGAACCTGACAGAGAGAAACGAGCAATTTTCCCGGCGCTGATTTATTC 794

Db	636	ANTGCTGGTAGAAATGCCCGAGGAGAGAAATGAGCCCATATATCCCTGCCCTGATATACTC	695
QY	795	GTCTG 799	
Db	696	ATCTG 700	
RESULT 20			
AI675803			
LOCUS	AI675803	661 bp	linear EST 17-DEC-1999
DEFINITION	wb97a12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2313598 3'		
ACCESSION	AI675803		similar to SW:PSN2_HUMAN P49810 PRESENILIN 2 ; mRNA sequence.
VERSION	AI675803.1	GI:4876283	
KEYWORDS			EST.
SOURCE			human.
ORGANISM			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS			1 (bases 1 to 661)
TITLE			NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL			National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT			Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. DNA Sequencing by: Greg Lennon, Ph.D. Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1317 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 461. Location/Qualifiers 1. .661 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2313598" /clone_lib="NCI_CGAP_Pr28" /sex="male" /dev_stage="adult" /lab_host="DH10B" /note="Organ: prostate; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaudo."
FEATURES			
source			
BASE COUNT	132 a	190 c	166 g 171 t
ORIGIN			
Query Match	14.6%	Score 219;	DB 9; Length 661;
Best Local Similarity	59.5%	Pred. No. 1.9e-28;	
Matches 388;	Conservative	0; Mismatches 261;	Indels 3; Gaps 1;
QY	148	CTGAATACGGAGCATCTCACGTTATTCATCTATTGTGCGGGTGTCACATGATGGCT	207
Db	8	CTCAATACGGAGCGAGACATGATCATGCTGTTTGGTCCTGTCACATCTCTGTCATGATC	67
QY	208	CTGGTGTGTTTTACGATGACACGATTACGTTTTTATAGTCAAAACATGGAAGCATTTA	267
Db	68	GTGGTGTGACCCACCATCAAGTCTGTGGCTTCTACACAGAGAAGATGGACAGC	124
QY	268	CTATCATCATCTTTTTCGCGGGAACAGACAGATATCTGTTGAGAGGGGATTCATGTCATT	327
Db	125	ATCTACACGCCATTCATCTAGCAGACACACCTCGGTGGGCCAGCGCTCTCTCAACTCCGTG	184

Db 31 AAGGATGGGAGCACTAATCTATACCCCATTCACAGAAGATACCGAGACTGTGGCCAGAGA 90
Qy 313 GGATTGATGTCACCTGGAAATGCTCGTCATGTTTGGTGGTTCCTGATGACAGATT 372
Db 91 GCCCTGCACCTCAATCTGAATGCTGCCATCATGATCAGTGTGTTGTCATGACTATC 150
Qy 373 CTGCTGATTTCTTCTATATAACAGTTTATAAGCTTATTCATGATGATGGCTTATGTC 432
Db 151 CTCCTGGTGGTCTGTATATAACAGTGTATGAAGTCTATCCATGCTGGCTTATATATA 210
Qy 433 AGCAGTTTCT 492
Db 211 TCATCTCTATGTTGCTGCT 270
Qy 493 TTCGATGTCCTCCAGCGCACTATTGGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 552
Db 271 TATAACGTTCTGTGGACTACATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 330
Qy 553 GGAATGATGTCATACATTCGAAAGTCCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
Db 331 GGAATGATTTCCCATTCACCTGGAAGGTCCACTTCGACTCCAGCAGGCATATCTCATATG 390
Qy 613 ATGCTGCACCTAATGGCTCTGCT 672
Db 391 ATTAGTCCCTCATGGCCCTGGTGTATCAAGTACCTCCCTCAATGGACTGCTGGCTC 450
Qy 673 GTGCTGTTGTTATCTCGGTTTGGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
Db 451 ATCTTGGCTGTGATTTTCAAGTATGATCTAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 510
Qy 733 AGATATTGGTGGAACTGCACAGGAGAGAAAGAGCCCAATTTTCCGGGCGCTGATTTAT 792
Db 511 CGTATGCTGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTCCAGCTCTCATTTAC 570
Qy 793 TCGTC 797
Db 571 TCCTC 575

RESULT 27
AW850631 733 bp mRNA linear EST 19-MAY-2000
LOCUS IL3-CT0219-160200-063-A06 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW850631
VERSION AW850631.1 GI:7946148
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 733)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-IL3-CT0219-160
200-063-A06et3-2000-02-16et4-1)

Seq primer: puc 18 forward
High quality sequence stop: 635.
Location/Qualifiers
source 1..733
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0219"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 188 a 151 c 174 g 219 t 1 others
ORIGIN

Query Match 13.6%; Score 204.2; DB 10; Length 733;
Best Local Similarity 60.9%; Pred. No. 6.5e-26;
Matches 332; Conservative 0; Mismatches 213; Indels 0; Gaps 0;
Qy 253 AATGGAAGGCATTTACTATCATCATCTCTTTTGTCCGGGAAACAGACAGTATCGTTGAGAAG 312
Db 31 AAGATGGGAGCTATCTATACCCCATTCACAGAAGATACCGAGACTGTGGCCAGAGA 90
Qy 313 GGATTGATGTCACCTGGAAATGCTCTCGTCATGTTTGTGCGTGGTTCGTTCTGATGACAGATT 372
Db 91 GCCCTGCACCTCAATCTGAATGCTGCCATCATGATCAGTGTGTTGTCATGACTATC 150
Qy 373 CTGCTGATGTTTCTATATAACAGTTTATAAGCTTATTCATGATGATGGCTTATGTC 432
Db 151 CTCCTGGTGGTCTGTATATAACAGTGTCTAAGGTCTATCCATGCTGGCTTATATATA 210
Qy 433 AGCAGTTTCT 492
Db 211 TCATCTCTATGCTGCTGCT 270
Qy 493 TTCGATGTCCTCCAGCGCACTATTGGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 552
Db 271 TATAACGTTCTGTGGACTACATCTACTGTTGCACTCCTGATCTCGAATTTTGGTGGTG 330
Qy 553 GGAATGATGTCATACATTCGAAAGTCCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
Db 331 GGAATGATTTCCCATTCACCTGGAAGGTCCACTTCGACTCCAGCAGGCATATCTCATATG 390
Qy 613 ATGCTGCACCTAATGGCTCTGCT 672
Db 391 ATTAGTCCCTCATGGCCCTGGTGTATCAAGTACCTCCCTCAATGGACTGCTGGCTC 450
Qy 673 GTGCTGTTGTTATCTCGGTTTGGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
Db 451 ATCTTGGCTGTGATTTTCAAGTATGATTTAGTGGCTGTTTGTGTCGGAAGGTCCACTT 510
Qy 733 AGATATTGGTGGAACTGCACAGGAGAGAAAGAGCCCAATTTTCCGGGCGCTGATTTAT 792
Db 511 CGTATGCTGTTGAAACAGCTCAGGAGAGAAATGAAACGCTTTTCCAGCTCTCATTTAC 570
Qy 793 TCGTC 797
Db 571 TCCTC 575

RESULT 28
AW367465 613 bp mRNA linear EST 04-FEB-2000
LOCUS MR0-HT0164-081199-007-c09 HT0164 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW367465
ACCESSION AW367465
VERSION AW367465.1 GI:6872115
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Qy	613	ATGCTGCAC	TAATGGCTCTGGCTTTATCAAGTACCTACAGAAATGAC	TGTGTGGTTT	672
Db	391	ATTAGTCCCT	CATGGCCCTGGTATTCAAGTACCTCCCTGAATGAC	TGCTGGCTC	450
Qy	673	GTGCTGTTT	TATCTCGGTTTGGGATCTGGTTCCTGCTCACACAAAGGACCA	ATTG	732
Db	451	ATCTTGCT	GTGATTTTCAGTATATGATTTAGTGGCTGTTTTGTCTCGAAAGGTCCCACTT		510
Qy	733	AGATATTT	TGTTGGAACCTGCACAGGAGAGAAACGAGCCAATTTTCCCGGCGCTCAT	TATAT	792
Db	511	CGTATGCT	GTGTGAACACAGCTCAGGAGAGAAATGAAACGCTTTTCCAGCTCTCAT	TTATAC	570
Qy	793	TCGTC	797		
Db	571	TCCTC	575		

RESULT 33
AWB50727
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

AWB50727
IL3-CT0219-160200-064-H05 CT0219
AWB50727
AWB50727.1
EST.
human.

573 bp
mRNA
linear

EST 19-MAY-2000
Homo sapiens cDNA, mRNA sequence.

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 573)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
 Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
 Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bal, G. S., Simpson, D. H.,
 Bruntstein, A., de Oliveira, P. S., Bucher, P., Jongseil, C. V., O'Hare,
 M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
 Simpson, A. J.

TITLE	Simpson,A.O. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A. J. G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=IL3-CT0219-160>)
200-064-H058t3-2000-02-16t54-1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 481.

```

FEATURES
source
Location/Qualifiers
1. .573
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0219"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

```

BASE COUNT	130 a	127 c	127 g	189 t
ORIGIN				
Query Match		13.5%;	Score 202.2;	DB 10;
Best Local Similarity		60.7%;	Pred. No. 1.6e-25;	Length 573;

Matches	349;	Conservative	0;	Mismatches	223;	Indels	3;	Gaps	1;
QY	223	ATGAACACAGATACGTTTATAGTCAAAACAATGGAGGCATTTACTATACATCCCTCTTT	282						
Db	2	ATGAAGCAATACAGCTTTTATACCGGAAGATG--GGCAGCTAATCTATACCCCATTC	58						
QY	283	GTCGGGAACACAGACAGTATCGTTTGAGAGGGATTGATGTCACTTGGAAATGCTCGTCG	342						
Db	59	ACAGAAGATACCGAGACTGTGGGCCACAGAGCCCTGCACCTCAATTCTGAATGCTGCATC	118						
QY	343	ATGTTGTGCGTGGTCTTGATGCACAGTTCTGCTGATTTCTTCTATAAATACAAGTTT	402						
Db	119	ATGATCAGTGTCATGTTGTGCATGCATPCTCCTCGTGGTCTGTATAAATACAGATGC	178						
QY	403	TATAAGCTTATTATCATGGATGGCTTATTGTGACAGAGTTTCTTCTCTTTTCTCTATTCAC	462						
Db	179	TATAAGTTCATCCATGCTGGCTTATTATATCATCTCTATTGTTGCTGTTCTTTTTC	238						
QY	463	ACAATCTATGTGCACAGAGTTCTGAAAGTTTCGATGTGTCCCAAGCGCATTTGGTT	522						
Db	239	TTCATTTACTTGGGGGAAGTGTTTAAACACCTATAACGTTGCTGTGACTACATACTGTT	298						
QY	523	TTGTTTGGACTGGTAACTATGAGATTCTCGGAATGATGTGTATACATTGGAAGGTCCA	582						
Db	299	GCACCTCTGATCGGAATTTGGTGTGGGGAATGATTTCCATTCACCTGGAAGGTCCA	358						
QY	583	TTGGGCTGCAACAGTTCTACCTTATTACAATGCTGCACATAATGGCTCTGGTCTTTATC	642						
Db	359	CTTCGACTCCACAGGCATATCTCAATTATGATTAGTGCCCTCATGSCCCTGGTGTATC	418						
QY	643	AAGTACCTACAGAAATGGACTGTGGTTTGCTGTTTGTATCTCGGTTTGGGATCTG	702						
Db	419	AAGTACCTCCTCAATGGAGCTGGGTGGCTCATCTTGGCTGTGATTTCAATATATGATTA	478						
QY	703	GTTGCCGTGCTCACACCAAAAGACCACTTGGATATTTGGTGGAACTGCACAGAGAGA	762						
Db	479	GTGCTGGTTGTGTCGGAAGTCCACTTCGTATGCTGTTGGAACAGCTCAGGAGAGA	538						
QY	763	AACGAGCCAATTTCCGGGGCGTGAATTAATGCTG	797						
Db	539	AATGACACGCTTTTTCGAGCTCTCAATTTACTCTCTC	573						

RESULT 34	REFERENCE
AW604307	AUTHORS
LOCUS	TITLE
DEFINITION	JOURNAL
ACCESSION	COMMENT
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 601)
HCGP <http://www.ludwig.org.br/ORESTES>.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?c1=IL3&t2=IL3-CT0219-280100-062-D09&t3=2000-01-28&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 600.
Location/Qualifiers

FEATURES

```

source
1..601
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0219"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT   138 a   128 c   135 g   199 t     1 others
ORIGIN
~
Query Match      13.4%; Score 201.6; DB 10; Length 601;
Best Local Similarity 60.6%; Pred. No. 2e-25;
Matches 330; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

QY    253 AATGGAAGCAATTACTATCATACCTTTTGTCCGGGAACAGACAGATCGTTGAGAAG 312
Db    31  AAGGATGGCAGCTAATCTATACCOCATTCACAGAAGATACCGAGACTGTGGGCCACAGA 90
QY    313 GAATGATGTCACCTTGGAAGGCTCTGCTCATGTTGTCGGTGCTGTTCTGATGACAGTT 372
Db    91  GCCCTGCACTAATCTCTGAATGCTGCCATCATGATCAGTGTCTGTTGTCATGACATC 150
QY    373 CTGCTGATTTTCTTATAAAATACAAGTTTATTAAGCTTATTCATGGATGCTATTGTC 432
Db    151 CTCCTGGTGCTGTATATAATACAGGTGCTATTAAGTTCATCCATGCCCTGCTATTATA 210
QY    433 AGCAGTTTCTTTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 492
Db    211 TCATCTCTATTGTTGCTGTTCTTTTTCATTCATTTACTTGGGGAGAGTGTTTAAACC 270
QY    493 TTCGATGTCCTCCAGCGCACTATTGGTTTGTGGACGTGGGTAACTATFGAGTCTC 552
Db    271 TATAAGTTGCTGTGGACTACATTTACTGTGCACCTCTGATCTGGAATTTTGGTGGTG 330
QY    553 GGAATGATGCTATCATTTGGAAGGCTCCATTTGCTGCAACAGTTCCTACCTATTATACA 612
Db    331 GGAATGATTTCCATTCATCTGGAAGAGTCCACTTCGACTCCAGAGGCATATCTCATTTG 390
QY    613 ATGCTGCACTAATGGCTGTGCTTTTATCAAGTACCTACCAGAAATGACACTGTGTGTTT 672
Db    391 ATTAGTGCCTCATGSCCCTGTGTTTATCAAGTACCTCCCTGAATGACACTGCGTGCCTC 450
QY    673 GTGCTGTTGTTATCTCGGTTTGGGATCTGGTTGCGGTGCTCACACCAAAGGACCAATTG 732
Db    451 ATCTTGGCTGTGATTTCAATATGATTTAGTGGCTGTTTGTGTCGCAAGGTCCTACTT 510
QY    733 AGATATTTCGTGAACTCCACAGAGAGAAGACCAATTTCCGCGCGCTCATTTAT 792
Db    511 CGTAGCTGTTGAAACAGCTCANGAGAGAATGAACGCTTTTCCAGCTCTCATTTAC 570
QY    793 TCCTC 797
Db    571 TCCTC 575

RESULT 35
AW850572
LOCUS IL3-CT0219-160200-060-H02 CT0219 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW850572
ACCESSION AW850572
VERSION AW850572.1 GI:7946089
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 757)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

```

```

Db      419  GTGCCCTCATGGCCCTGGTGTATATCAAGTACCTCCCTGAATGAGCTGGCTGCTCACT 478
Qy      677  TGTTGTTTACTCGGTTTGGGATCTGTTGCCGTGCTCACACCAAGGACCATTGGAGAT 736
Db      479  TGGCTGTGATTTACAGTATATGATTTAGTGGCTGTTTGTGTCGGAAGGCTCCACTTCGTA 538
Qy      737  ATTGTGTGGAACCTGCACAGAGAGAACAGCAATTTTCCCGGCGCTGATTTATTCGT 796
Db      539  TGGCTGTGGAACAGCTCAGAGAGAAATGAACGCTNTTCCAGCTCTCATTTACTCCT 598
Qy      797  C 797
Db      599  C 599

```

```

RESULT 36
AW850573
DEFINITION IL3-CT0219-160200-060-H03 CT0219 Homo sapiens mRNA linear EST 19-MAY-2000
ACCESSION AW850573
VERSION AW850573.1 GI:7946090
KEYWORDS EST.
SOURCE human.

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 593)

```

```

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

```

Shotgun sequencing of the human transcriptome with ORF expressed

```

TITLE sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663

```

```

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-IL3-CT0219-160200-060-H03&t3=2000-02-16&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 6

High quality sequence stop: 532.

Location/Qualifiers

1..593

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="CT0219"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site:1; Sma1; Site:2; Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

135 a 130 c 130 g 197 t 1 others

```

BASE COUNT 135 a 130 c 130 g 197 t 1 others
ORIGIN
Query Match 13.4%; Score 201.4; DB 10; Length 593;
Best Local Similarity 60.4%; Pred. No. 2.2e-25;
Matches 350; Conservative 0; Mismatches 226; Indels 3; Gaps 1;

```

```

Qy      219  TACGATGAACACGAGTATACGTTTATAGTCAAAACAATGGAAGGCAATTTACTATACATCC 278
Db      9      TACCATTAACTCAGTACGCTTTTATAGTCCGAAGGATGGTTAGC---TAATCTATACCCC 65
Qy      279  TTTTGTCCGGGAACACAGACAGTATCGTTGAGAAGGATTGATGTCACCTTGGAAATGCTCT 338
Db      66  ATTACACAGAAGATACCGAGACTGTTGGCCAGAGAGCCCTGCACCTCAATTCGAATGCTGC 125
Qy      339  CGTCATGTTTGGTGGTGGTCTGCTGATGACAGATTTCTGCTGATTTCTTCTTATATAATACAA 398
Db      126  CATCATGATCAGTGTCAATGTTGTCAATGACTACCTCTCTGTTGTTCTGTATAAATACAG 185
Qy      399  GTTTTATAAGCTTATTCATGATGGCTTATTTGTCAGCAGTTTTCTTCTTCTTCTTCTTCTT 458
Db      186  TGCCTATAAGGTCATCCATCGCTGGCTTATATATATCATCTCTATTTGGTGTCTTCTTTT 245
Qy      459  CACTACAACTATGTGCAAGAAGTTCTGAAAAGTTTTCGATGTGCTCTCCAGCGCACTATT 518
Db      246  TTCATTCATTTACTTGGGGAAGTGTTTAAACCTATAACGTTGCTCTGGACTACATATAC 305
Qy      519  GGTTTTGTGGTGGTGGTAACTATGAGTTCCTCGGAATGATGTGTATACATTTGGAAGG 578
Db      306  TGTTCACACTCTCATCTGGAATTTTGGTGTGGTGGGAATGATTTCCATTCTACCTGGAAGG 365
Qy      579  TCCATTGCGCTCCACAGACTTCTACCTTATTAACAATGCTGCACACTAATGGCTCTGGTCT 638
Db      366  TCCACTTCGACTCCAGCAGGCATATCTCATTTATGATAGTAGTCCCTCATGSCCCTGGTGT 425
Qy      639  TATCAAGTACTACCAAGATGAGCTGTGTGTTTGTGCTGCTGTTGTTATCTCGGTTTGGGA 698
Db      426  TATCAAGTACTCCCTCCGTAATGGACTCGGTGGCTCATCTTGGCTGTGATTTTCAGTATATGA 485
Qy      699  TCTGTTGGCGTCTCACACCAAGGACCATTTGAGATATTTGCTGGAACACTGCACAGGA 758
Db      486  TTTAGTGGCTGTTTGTGTCGGAAGTCCACCTTCGTATGCTGTTGGAACACCTCACGA 545
Qy      759  GAGAAACGAGCCAAATTTTCCGGCGCTGATTTATTCGTC 797
Db      546  GAGAAATGAACCGCTTTTCCAGCTCTCATTTACTCCTC 584

```

```

RESULT 37
AW604231
LOCUS

```

```

DEFINITION IL3-CT0219-210100-059-C05 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW604231
VERSION AW604231.1 GI:7308972
KEYWORDS EST.
SOURCE human.

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 599)

```

```

REFERENCE HCGP http://www.ludwig.org.br/ORESTES.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
TITLE Unpublished (1999)
JOURNAL Laboratory of Cancer Genetics
COMMENT Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0219-210100-059-C05&t3=2000-01-21&t4=1>)

Seq primer: puc 18 forward

High quality sequence stop: 563.

Location/Qualifiers

1..599

/organism="Homo sapiens"

```
/db_xref="taxon:9606"
/clone_lib="CT0219"
/dev_stage="Adult"
/notes="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 137 a 128 c 134 g 199 t 1 others
ORIGIN
Query Match 13.4%; Score 201.4; DB 10; Length 599;
Best Local Similarity 60.9%; Pred. No. 2.2e-25;
Matches 328; Conservative 0; Mismatches 211; Indels 0; Gaps 0;
Qy 253 AATGGAAGGAGTTTACTATACATCCCTTTTGTCCGGAAACACAGATATCGTTGAGAG 312
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
31 AAGGATGGCAGCTAATCTATACCCATTCCACAGAGATACCGAGACTGTGGCCAGAGA 90
Qy 313 GGATTGATGTCACCTGGAAATGCTCTGTCATGTTGTGCGTGGTCTCTGATCAGAGTT 372
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
91 GCCCTGCACCTCAATCTGAATGCTGCCATCATGATCAGTGTCTATGTTGTCATGACTATC 150
Qy 373 CTGCTGATTTGTTTCTATAAACAAGCTTTTATAAGCTTTATCATGGATGGCTTATGTC 432
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
151 CTCTGCTGTTCTGTATANAATACAGGTGCTATAAGGTCCATCCGCTGGCTTATATA 210
Qy 433 AGCAGTTTCTCTCTTTTCCATATTCACATACATATGTCGAAGAAGTCTGAAAGT 492
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
211 TCATCTCTATTTGTTGCTGTTCTTTTTCATTCATTTACTTGGGGAAAGTCTTAAACC 270
Qy 493 TTCGATGTCCTCCCGCAGCTATGTTGTTTGGACTGGTGAATGAGTCTC 552
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
271 TATACCTGCTGCTGGGACTACATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 330
Qy 553 GGAATGATGATATACATTTGGAAGGTCATTTGCGTCTGCAACAGTTTCTACCTATTACA 612
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
331 GGAATGATTTCCATCTACTGGAAGGTCCTACTCGAGTCCAGCAGGATATCTCATATG 390
Qy 613 ATGCTCGCATATGCTCTGCTTTTATCAAGTACCTACAGATGAGTGTGTTGTTT 672
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
391 ATTAGTCCCTCATGCGCCCTGGTGTATCAAGTACCTCCCTGAAAGTGGCTGCTC 450
Qy 673 GTGCTGTTGTTATCTCGGTTGGGATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 732
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
451 ATCTTGCTGTGATTTTCAATATATGATCTAGTGTGCTGTTTGTGTCGAAAGTCCACTT 510
Qy 733 AGATATTTTGTGGAAGTGCAGGAGAGAAACAGGCCAATTTTCCGCGGCTGATTTA 791
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
511 CGTATGCTGTTGGAACAGCTCAGGAGAGAAATGAAACGCTTTTTCAGCTCTCATTTA 569
RESULT 38
AW850632/c 737 bp mRNA linear EST 19-MAY-2000
LOCUS IL3-CT0219-160200-063-B04 CT0219 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW850632
ACCESSION AW850632.1 GI:7946149
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 737)
REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
```

```

RESULT 39
AW850712      581 bp      mRNA      linear      EST 19-MAY-2000
DEFINITION    IL3-CT0219-160200-064-C06 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION     AW850712
VERSION       AW850712.1 GI:7946229
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 581)
AUTHORS       Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
               Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
               Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
               Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
               M.J., Soares,F., Brentani,R., Reis,L.F., de Souza,S.J. and
               Simpson,A.J.
TITLE         Shotgun sequencing of the human transcriptome with ORF expressed
               sequence tags
JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE       20202663
COMMENT       Contact: Simpson A.J.G.
               Laboratory of Cancer Genetics
               Ludwig Institute for Cancer Research
               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
               Brazil
               Tel: +55-11-2704922
               Fax: +55-11-2707001
               Email: asimpson@ludwig.org.br
               This sequence was derived from the FAPESP/LICR Human Cancer Genome
               Project. This entry can be seen in the following URL
               (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=IL3-CT0219-160
               200-064-C06&t3=2000-02-16&t4=1)
               Seq primer: puc 18 forward
               High quality sequence stop: 560.
               Location/Qualifiers
                 1..581
                   /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /clone_lib="CT0219"
                   /dev_stage="Adult"
                   /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                   SmaI; A mini-library was made by cloning products derived
                   from ORESTES PCR (U.S. Letters Patent application No. 196
                   ,716 - Ludwig Institute for Cancer Research) profiles
                   into the puc 18 vector. Reverse transcription of tissue
                   mRNA and cDNA amplification were performed under low
                   stringency conditions."
BASE COUNT    135 a 128 c 126 g 192 t
ORIGIN
Query Match      13.3%; Score 200; DB 10; Length 581;
Best Local Similarity 60.5%; Pred. No. 3.9e-25;
Matches 329; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

QY 253 AATGGAAGCATTACTATACATCCTTTTGTCCGGGAACAGACAGATCGTTGAGAAG 312
Db 31 AAGGATGGCGAGCTAATCTATACCCATTACACAGAAGATACCGAGACTGTGGCCACAGAGA 90

QY 313 GGATTGATGTCATTGGAATGCTCTCGTCATGTTGTGGTGGTCTGTCATGACAGTT 372
Db 91 GCCTGCATCAATCTGAATGTCGCATCATCATGATGTCATGTTGTGTCATGACATC 150

QY 373 CTGCTGATTTTCTTATTAATAACAAGTTTATTAAGCTTATTCATGATGGCTTATTGTC 432
Db 151 CTCTGGTGGTCTGTATATAATACAGGTGCTATAAGTATCATCCATCGCTGGCTTATATA 210

QY 433 AGCAGTTTCTCTCTTTCCCTATTACATACATATGTCGAAGAAGTCTGAAAGT 492
Db 211 TCATCTCTATTGTTGCTTCTTTTTCATTTCATTTACTTGGGGAAGTGTTTAAACC 270

```

```

QY 493 TTCGATGTCCTCCAGCGCACTATTGGTTTGTGTTGGACTGGGTAACATATGAGTTC 552
Db 271 TATAACGTTGCTGTGACTACATTTACTGTGCACTCCTGATCTGGAATTTTGTGTGGTG 330

QY 553 GGAATGATGTTATACATTTGGAAGTCCATTCGCTCTGCAACAGTTCCTACCTTATACA 612
Db 331 GGAATGATTTCCATTCCAGTGAAGGTCCACTTCGACTCCAGCAGCATATCTCATATG 390

QY 613 ATGTCCTGCAATAAGTCTCTGTTTATCAAGTACCTACCAAGATGGAGTGTGGTTT 672
Db 391 ATTAGTGCCTCATGCGCTGTTTATCAAGTACCTCCCTGAATGGACCGCTGGCTC 450

QY 673 GTCGCTGTTGTTATCTCGGTTTGGGATCTGGTTCGCTCACACAAAGACCATG 732
Db 451 ATCTTGGCTGTGATTTCACTATATGTTAGTGGCTGTTTGTGTCGGAAGTCCACTT 510

QY 733 AGATATTTCGTGAACTCCAGGAGAGAGAAAGCCCAATTTCCCGCGCTGATTTAT 792
Db 511 CGTATGCTGTTGAAACAGCTCAGGAGAGAAATGAACGCTTTTCCAGCTCTCATTTAC 570

QY 793 TCGT 796
Db 571 TCCT 574

RESULT 40
AW376912      585 bp      mRNA      linear      EST 04-FEB-2000
LOCUS         IL3-CT0219-271099-022-C05 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION     AW376912
VERSION       AW376912.1 GI:6881575
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 585)
AUTHORS       HCGP http://www.ludwig.org.br/ORESTES.
               The FAPESP/LICR Human Cancer Genome Project
               Unpublished (1999)
JOURNAL       Contact: Simpson A.J.G.
               Laboratory of Cancer Genetics
               Ludwig Institute for Cancer Research
               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
               Brazil
               Tel: +55-11-2704922
               Fax: +55-11-2707001
               Email: asimpson@ludwig.org.br
               This sequence was derived from the FAPESP/LICR Human Cancer Genome
               Project. This entry can be seen in the following URL
               (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0219-
               271099-022-C05&t3=1999-10-27&t4=1)
               Seq primer: puc 18 forward
               High quality sequence start: 11
               High quality sequence stop: 546.
               Location/Qualifiers
                 1..585
                   /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /clone_lib="CT0219"
                   /dev_stage="Adult"
                   /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                   SmaI; A mini-library was made by cloning products derived
                   from ORESTES PCR (U.S. Letters Patent application No. 196
                   ,716 - Ludwig Institute for Cancer Research) profiles
                   into the puc 18 vector. Reverse transcription of tissue
                   mRNA and cDNA amplification were performed under low
                   stringency conditions."
BASE COUNT    135 a 127 c 126 g 197 t
ORIGIN
Query Match      13.3%; Score 200; DB 10; Length 585;
Best Local Similarity 60.5%; Pred. No. 3.9e-25;

```


Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-IL3-CT0219-160
200-060-A068t3-2000-02-16t4-1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 480.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source
1..591
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0219"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
136 a 128 c 130 g 196 t 1 others

Query Match 13.3%; Score 198.8; DB 10; Length 591;
Best Local Similarity 60.2%; Pred. No. 6.3e-25;
Matches 328; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 253 AATGGAAGGCAATTACTATACATCCTTTTGTCCGGGAACACAGACAGATCGTTGAGAAG 312
DB 34 AAGGATGGCCAGTAATCTATACCCCATTCACAGAAGATACCGAGACTGTGGCCAAAGA 93
QY 313 GGATGATGTCACCTTGGAAATGCTCTCGTCATCTTGTGGTGTGCTTCTGTGATGACAGTT 372
DB 94 GCCTGCACCTCAATCTGAATGTGCGCATCATCATGATGATGTCATTTGTCATGACTATC 153
QY 373 CTGCTGATGTTTCTTATATAACAAAGTTTATAAGCTTATTCATGATGGCTTATGTC 432
DB 154 CTTCTGTGTGTTCTGTATATAACAGTGTCTAAGGTCATCCATCGCTGGCTTATATA 213
QY 433 AGCAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 492
DB 214 TCATCTATGTTGTGTTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 273
QY 493 TTGCGATGTGCTCCAGCGCACTATTGGTTTGTGGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCT 552
DB 274 TATAAGCTGCTGTGACTACATTTACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 333
QY 553 GGAATGATGTTATACATTTGGAAGTCCATTCGCTGCTGCAACAGTTCTACCTTATATACA 612
DB 334 GGAATGATTTCCATTTCACTGGAAGTCCACTTCGACTCCAGCAGGCATATCTCAATTATG 393
QY 613 ATGCTGCACATATGCTCTGGTCTTTATCAAGTACTTACCAGATGGAGTGTGGTTT 672
DB 394 ATTAGTGCCTCATGCGCCCTGGTGTATCAAGTACTTCCCTGAAATGGAGTGGCTGGCTC 453
QY 673 GTGCTGTGTTGTTATCTCGGTTTGGGATCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 732

Db 454 ATCTTGCGTGTGATTTTCAGTATATGATTTAGTGGCTGTTTGTGTCGGAAGGTCCACTT 513
QY 733 AGATATTGTGGAAACTGCACAGGAGAGACGCAATTTTCCCGCGCTGATTTAT 792
Db 514 CGTATGCTGGTTGAACAGCTCAGGAGAGAAATGANNACGGTTTTTCCAGCTCTCATTTAC 573
QY 793 TCCTC 797
Db 574 TCCTC 578

RESULT 43
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW367429 588 bp mRNA linear EST 04-FEB-2000
MR0-HT0164-211099-003-e03 HT0164 Homo sapiens cDNA, mRNA sequence.
AW367429
AW367429.1 GI:6872079
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0t2-MR0-HT0164-211099-003-e03t3-1999-10-21t4-1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 503.

FEATURES
source
1..588
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0164"
/dev_stage="Adult"
/note="Organ: head neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
136 a 126 c 137 g 189 t

BASE COUNT
ORIGIN
Query Match 13.2%; Score 198.6; DB 10; Length 588;
Best Local Similarity 60.4%; Pred. No. 6.8e-25;
Matches 327; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

QY 257 GAAGGCATTACTATACATCCCTTTTGTCCGGGAACACAGACAGATCGTTGAGAAGGAT 316
Db 15 GATGGCAGCTAATCTATACCCCATTCACAGAAGATACCGAGACTGTGGCCAGAGACCC 74
QY 317 TGATGTCACCTGGAATGCTCGTCATGTTGCGTGTGCTTCTGATGACAGTTCGTC 376
Db 75 TGCACCTCAATTCGAATGCTGCCATCATGATCAGTGTGTTGTCATGACTATCCTCC 134
QY 377 TGATTTCTTTTCTATAAATACAAAGTTTATAAGCTTATTCATGATGGCTTATTTGACGA 436
Db 135 TGGTGGTTCGTATATAATACAGGTGCTATAGGTCATCCATCGCTGGCTATTATATCAT 194

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=st3-IL3-Cr0219-160
200-064-D10st3-2000-02-16st4-1)
Seq primer: puc 18 forward
High quality sequence stop: 569.
Location/Qualifiers
1. 570
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0219"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 131 a 123 c 126 g 190 t
ORIGIN

Query Match 13.2%; Score 198.2; DB 10; Length 570;
Best Local Similarity 60.5%; Pred. No. 8.1e-25;
Matches 326; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 253 AATGGAAGGCATTTACTATACATCCCTTTTGTCCGGGAACAGACAGTATCGTTGAGAAG 312
DB 31 AAGCATGGCAGCTAACTATACCCCATTCACAGAAGATACCGAGAGCTGGGGCAGAGA 90
QY 313 GGATTGATGCACCTTGAATGCTCTCGTCATGTTGTGGTGGTCTTGATGACAGATT 372
DB 91 GCCCTGCACCAATCTCGAATGCTGCCATCATGATCAGTGTCAATGTGTCATGACATC 150
QY 373 CTGCTGATTTCTTCTATAAACAAGTTTATAAGCTTATTCATGATGGCTTATTGTC 432
DB 151 CTCCTGGTGTCTGTATAAATACAGTGTCTATAAGTCAATCCATGCTGCTTATTATA 210
QY 433 AGCAGTTTTCTCTTTCTTCTATTCACATCAATCTATGTGCAAGAGTTCTGAAAAGT 492
DB 211 TCATCTCTATTGTTGCTGTTCTTTTTCATTCATCTTACTTGGGGAGTGTTTAAACC 270
QY 493 TTCATGTGCTCCAGCGCACTATGTTTGTGGATGGGTAACTATGAGTCTC 552
DB 271 TATAACGTGTGCTGGGACTACATCTACTGTCCTGATCTGGAATTTTGGTGTGGT 330
QY 553 GGAATGATGTGTATACATGGAAGGTCATGCTGCTGCAACAGTCTACCTTATTACA 612
DB 331 GGAATGATTTCCATCTACTGGAAGGTCCTGCTGCTGCAAGGATATCTCATTTATG 390
QY 613 ATGCTGCACATAATGGCTCTGGCTTTTATCAAGTACCTACCAAGTGGTGTGGTTT 672
DB 391 ATTAGTGCCTCATGGCCCTGGTGTATCAAGTACCTCCCTGAATGAGTGGCTGCTC 450
QY 673 GTGCTGTTTGTATCTCGGTTTGGGATCTGGTTCGCTGCTCACCACAAAGGACCAATG 732
DB 451 ATCTTGGCTGTGATTTTCAGTATATGATTTAGTGGCTGTTTGTGTCGGAAGGTCAC 510
QY 733 AGATATTTGGTGGAAATGTCACAGAGAGAAACGAGCAATTTTCCCGGCGCTGATTTA 791
DB 511 CGTATGCTGGTGGAAACAGCTTAGAGAGAAATGAACGCTTTTCCAGCTCTCATTTA 569

RESULT 46
AW850639
LOCUS 614 bp mRNA linear EST 19-MAY-2000
DEFINITION IL3-CT0219-160200-063-D11 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW850639
VERSION AW850639.1 GI:7946156
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 614)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=st3-IL3-Cr0219-160
200-063-D11st3-2000-02-16st4-1)
Seq primer: puc 18 forward
High quality sequence stop: 486.
Location/Qualifiers
1. 614
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0219"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 146 a 133 c 141 g 194 t
ORIGIN

Query Match 13.2%; Score 197.8; DB 10; Length 614;
Best Local Similarity 60.2%; Pred. No. 9.2e-25;
Matches 328; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

QY 253 AATGGAAGGCATTTACTATACATCCCTTTTGTCCGGGAACAGACAGTATCGTTGAGAAG 312
DB 31 AAGCATGGCAGCTAACTATACCCCATTCACAGAAGATACCGAGAGCTGGGGCAGAGA 90
QY 313 GGATTGATGCACCTTGAATGCTCTCGTCATGTTGTGGTGGTCTTGATGACAGATT 372
DB 91 GCCCTGCACCAATTTCTGAATGCTGCCATCATGATCAGTGTCAATGTGTCATGACATC 150
QY 373 CTGCTGATTTTCTTCTATAAACAAGTTTATAAGCTTATTCATGATGGCTTATTGTC 432
DB 151 CTCCTGGTGTCTGTATAAATACAGTGTCTATAAGTCAATCCATGCTGCTTATTATA 210
QY 433 AGCAGTTTTCTCTTTCTTCTTCTATTCACATCAATCTATGTGCAAGAGTTCTGAAAAGT 492
DB 211 TCATCTCTATTGTTGCTGTTCTTTTTCATTCATCTTACTTGGGGAGTGTTTAAACC 270

QY	493	TTCGATGTCTCCACGCCACTATTGGTTTTTTTGGACTGGGTAAGTCTCTC	552
Db	271	TATAACGTTGCTGGGACTACATTACTGATGCACCTCGATCTCGAATTTTGGTGCGTG	330
QY	553	GGAATGATGTGTATACATTGGAAAGGCCATTGGCTCTGCAACAGTTCTACCTTATTACA	612
Db	331	GGAATGATTCCATTCTACTGGAAGGTCCACTCCGACTCCAGCAGGCATATCTCATTTATG	390
QY	613	ATGCTCGCACTAATGGCTCTGGTCTTTATCAAAGTACCTACCAGAATGGACTGTGTGTTT	672
Db	391	ATTAGTCCCCTCATGGCCCTGGTGTATTCAAATACCTCCCTGAATGGACTGAGTGGCTC	450
QY	673	GTGCTGTTTGTATCTCGGTTTGGGATCTGGTTCGGCTGCACACCAAAAGGACCATTG	732
Db	451	ATCTTGCGCTGTGATTTTCAGTATATGATTTAGTGGCTGATGTGTCTCCGAAGGTCACCT	510
QY	733	AGATATTTTGGTGGAAACTGCACAGGAGAGAAAACGACCAATTTTCCCGGCGCTCATTTAT	792
Db	511	CGTATGCTGTTGAAACAGCTCAGGACAGAAATGAACGCTCTTTCCAGCTCTCATTTAC	570
QY	793	TCGTC	797
Db	571	TCGTC	575

RESULT	47
AW376998	
LOCUS	AW375998 584 bp mRNA linear EST 04-FEB-2000
DEFINITION	IL3-CT0219-161199-031-G03 CT0219 Homo sapiens cDNA, mRNA sequence.

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 584) HCGP http://www.ludwig.org.br/ORESTES . The FAPESP/LICR Human Cancer Genome Project Unpublished (1999) Contact: Simpson A.J.G.
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

BASE COUNT	136 a	128 c	128 g	192 t
ORIGIN				

Query Match 13.1%; Score 196.8; DB 10; Length 584;

[illegible]

RESULT	48
AW604233	
LOCUS	
DEFINITION	IL3-C70219-210100-059-c08 CT0219 Homo sapiens CDNA, mRNA sequence.
ACCESSION	AW604233
VERSION	AW604233.1
KEYWORDS	EST .
SOURCE	human.
	601 bp mRNA linear EST 23-MAR-2000

SOURCE Human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 601)
HCCP <http://www.ludwig.org.br/ORESTES>.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Simpson A.J.G.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 601)
HCPG <http://www.ludwig.org.br/ORESTES>.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asmpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0219-210100-059-C08&t3=2000-01-21&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 599.

RESULT 50
 AW367418
 LOCUS
 DEFINITION MR0-HT0164-211099-003-g03 HT0164 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW367418
 VERSION AW367418.1 GI:6872068
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 553)
 HCGP <http://www.ludwig.org.br/ORESTES>.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0st2-MR0-HT0164-211099-003-g03st3-1999-10-21st4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 28
 High quality sequence stop: 553.

FEATURES
 source
 1..553
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HT0164"
 /dev_stage="Adult"
 /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No.196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 125 a 120 c 127 g 181 t
 ORIGIN

Query Match 12.6%; Score 189.4; DB 10; Length 553;
 Best Local Similarity 61.0%; Pred. No. 2.7e-23;
 Matches 307; Conservative 0; Mismatches 196; Indels 0; Gaps 0;
 Qy 289 GAACACACAGTATCGTTGAGAGGGATTGATGTCACCTTGAATGCTCTCGTCATCTTG 348
 Db 50 GATACCGAGACTTGGGCCAGAGAGCCCTGACCTCAATCTGAATGCTGCCATCAGATC 109
 Qy 349 TGGCTGCTCGTCTGTGACAGTTCCTGCTGATTTCTTTCTATAAATACAAAGTTTATAAG 408
 Db 110 AGTGTCATTTGTGTCAGTACTATCTCTGCTGGTCTCTGTATAAATACAGTGCATAAG 169
 Qy 409 CTATTTCATGGATGGCTTATTGTCAGCAGTTTCTTCTTTCTTTTCCTATTCACTACAATC 468
 Db 170 GTCATCCATGCTGGTTTATTATATATCATCTCTATGTTGCTGTTCTTTTTCATTTCATT 229
 Qy 469 TATGTGCAAGAGTCTGAAAGTTTCGATGCTGCTCCAGCGCACTATTGGTTTGT 528
 Db 230 TACTTGGGGAAGTGTAAACCTATAACGTTCTGTGGACTACATTACTGTGCACTC 289
 Qy 529 GGACTGGGTAATGAGATTCTCGGAATGATGTATACATTGGAAGTCCATTGCGT 588
 Db 290 CTGATCTGGAATTGGGTGGTGGGAATGATTTCCATTACCTGGAAGTCCACTTGA 349
 Qy 589 CTGCAACAGTCTTACCTTATTACAATGCTGCACTAATGGCTCTGGTCTTTATCAAGTAC 648

Db 350 CTCACGACGCATATCTCATTTAGTATGATAGTCCCTCATGGCCCTGGTGTATATCAAGTAC 409
 Qy 649 CTACCCAGAATGGACTGTGTGCTGTCTGTTGTTTATCTCGGTTTGGGATCTGGTTGCC 708
 Db 410 CTCCTGAAATGGACTGCGTGGCTCATCTTGGCTGTGATTTCAAGTATATGATTTAGTGGCT 469
 Qy 709 GTGCTCACACCAAAAGACCAATTGAGATATTTGGTGGAAACTGCACAGGAGAGAAACGAG 768
 Db 470 GTTTGGTGTCCGAAACGCTCCACITTCGTATGCTGTGTTGAAACAGCTCAGGAGAGAAATGAA 529
 Qy 769 CCAATTTTCCCGGCGCTGATTTA 791
 Db 530 ACGCTTTTCCAGCTCTCATTTA 552
 Search completed: July 15, 2003, 07:02:29
 Job time : 2319 secs

